

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lawrence, Geoffrey

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Ratner & Prestia
- (B) STREET: P.O. Box 980
- (C) CITY: Valley Forge
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19482

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To be assigned
- (B) FILING DATE: Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 96 24677.2
- (B) FILING DATE: Filed November 27, 1996
and
- (A) APPLICATION NUMBER: GB 9709463.5
- (B) FILING DATE: May 9, 1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Prestia, Paul F.
- (B) REGISTRATION NUMBER: 23,031
- (C) REFERENCE/DOCKET NUMBER: GH30170

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-407-0700
- (B) TELEFAX: 610-407-0701
- (C) TELEX: 846169

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGCTGCC	180
TACCAACCAC	TGGATTCCCTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGCCAT	GAAGAACCCAG	GTTGCCCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCC	GCAGCCTTGG	TAACTATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAGCAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCCTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCC	CAGGCAGCTG	600
CTCACTTTCT	TCGAGAAGGC	CGCCGAGCCC	CACGCGCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCGCAACA	CCATCGCCCC	CAACTGCGCG	720
CTGCGCCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCGGCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGG	TTTCCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAACT	840
TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCCAACT	TTGTCAGCAA	TGTCAACACC	AGTGTGCT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCA	TAAGATGCGT	TTTCACAGCC	AACTCTCTC	CCAGGACTGG	1080
CCACACCCTA	CCTTGTGT	GATGGCACAC	CAGAATGAA	ACCCGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
1				5				10				15			
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
				20				25				30			
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
				35			40				45				
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
				50			55				60				
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
				65			70			75			80		
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
				85			90			95					
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
				100			105			110					
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
				115			120			125					
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
				130			135			140					
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
				145			150			155			160		
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
				165			170			175					
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
				180			185			190					
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala

195	200	205	
Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp			
210	215	220	
Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala			
225	230	235	240
Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe			
245	250	255	
Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys			
260	265	270	
His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys			
275	280	285	
Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe			
290	295	300	
Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly			
305	310	315	320
Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser			
325	330	335	
His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His			
340	345	350	
Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met			
355	360	365	
Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro			
370	375	380	
Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp			
385	390	395	400

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGATGCC	180
TACCACCACC	TGGATTCCTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGGCAT	GAAGAACCCAG	GTTGCCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCC	GCAGCCTTGG	TAACTATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAGCAAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCGTGCTC	CGGGCCCCAC	TGCCAGGCC	ACGTCTGCC	CAGGCAGCTG	600
CTCACTTTCT	TCGAGAAAGGC	CGCCGAGCCC	CACGCCAGG	GCCTGCTACT	GTGCCCATGT	660
CCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCCAACA	CCATGCC	CAACTGCGCG	720
CTGCCGCC	TGGCCCCCAA	CTGCCTGGAG	CTGCCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGG	TTTCCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAAC	840
TGTGCAACAG	AGCAGTCCAG	ATGTCCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCCAACT	TTGTCAGCAA	TGTCAACACC	AGTGTGCTC	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCAGC	TAAGATGCCT	TTTCACAGCC	AACTCTCTC	CCAGGACTGG	1080
CCACACCCCTA	CCTTGTGT	GATGGCACAC	CAGAATGAAA	ACCCGTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
1 5 10 15
Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
20 25 30
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
35 40 45
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Asp Ala Tyr His His Leu
50 55 60
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
65 70 75 80
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
85 90 95
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
100 105 110
Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
115 120 125
Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
130 135 140
Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
145 150 155 160
Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
165 170 175
Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
180 185 190
Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
195 200 205
Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
210 215 220
Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
225 230 235 240
Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
245 250 255
Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
260 265 270
His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
275 280 285
Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
290 295 300
Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
305 310 315 320
Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
325 330 335
His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
340 345 350
Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
355 360 365
Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
370 375 380
Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Ser Leu Trp

385

390

395

400

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGCGCCGGC	GCAACACCAT	CGCCCCAAC	TGCGCGCTGC	CGCCTGTGGC	CCCCAACTGC	60
CTGGAGCTGC	GGCGCCTCTG	CTTCTCCGAC	CCGCTTGCA	GATCACGCC	GGTGGATTTC	120
CAGACCCACT	GCCATCCCCT	GGACATCCTA	GGAACTTGTG	CAACAGAGCA	GTCCAGATGT	180
CTACGAGCAT	ACCTGGGCT	GATTGGGACT	GCCATGACCC	CCAACTTGT	CAGCAATGTC	240
AACACCAGTG	TTGCCTTAAG	CTGCACCTGC	CGAGGCAGTG	GCAACCTGCA	GGAGGGAGTGT	300
GAAATGCTGG	AAGGGTTCTT	CTCCCACAAAC	CCCTGCCTCA	CGGAGGCCAT	TGCAGCTAAG	360
ATGCGTTTC	ACAGCCAAC	CTTCTCCCAG	GACTGGCCAC	ACCCTACCTT	TGCTGTGATG	420
GCACACCAGA	ATGAAAACCC	TGCTGTGAGG	CCACAGCCCT	GGGTGCCCTC	TCTTTCTCC	480
TGCA	CCTGATTCT	GCTCCTGAGC	CTATGGTAG			519

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val
1				5				10				15			
Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu
				20				25				30			
Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp
				35				40			45				
Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr
				50				55			60				
Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Val	Ser	Asn	Val
				65				70			75			80	
Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu
				85				90			95				
Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys
				100				105			110				
Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe
				115				120			125				
Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met	Ala	His	Gln	Asn
				130				135			140				
Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro	Ser	Leu	Phe	Ser
				145				150			155			160	
Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Ser	Leu	Trp					
				165				170							

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lawrence, Geoffrey

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Ratner & Prestia
- (B) STREET: P.O. Box 980
- (C) CITY: Valley Forge
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19482

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To be assigned
- (B) FILING DATE: Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 96 24677.2
- (B) FILING DATE: Filed November 27, 1996
and
- (A) APPLICATION NUMBER: GB 9709463.5
- (B) FILING DATE: May 9, 1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Prestia, Paul F.
- (B) REGISTRATION NUMBER: 23,031
- (C) REFERENCE/DOCKET NUMBER: GH30170

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-407-0700
- (B) TELEFAX: 610-407-0701
- (C) TELEX: 846169

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCAACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGCTGCC	180
TACCAACC	TGGATTCCCTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGGCCT	GAAGAACCC	GTTGCCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCCT	GCAGCCTTGG	TAACTATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAAGAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCGTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCCT	CAGGCAGCTG	600
CTCACTTTCT	TCGAGAACGG	CGCCGAGCCC	CACGCGCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCGCAACA	CCATCGCCCC	CAACTGCGCG	720
CTGCCGCCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCGCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGG	TTTCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAACT	840
TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCCAACT	TTGTCAGCAA	TGTCAACACC	AGTGTGCT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCGC	TAAGATGCGT	TTTCACAGCC	AACTCTTCTC	CCAGGACTGG	1080
CCACACCCCTA	CCTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCTGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
1				5				10				15			
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
					20			25				30			
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
						35		40			45				
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
					50			55			60				
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
						65		70		75			80		
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
						85			90			95			
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
					100			105			110				
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
					115			120			125				
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
						130		135			140				
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
						145		150		155			160		
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
						165			170			175			
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
					180			185			190				
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala

195 200 205

Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
 210 215 220
 Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
 225 230 235 240
 Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
 245 250 255
 Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
 260 265 270
 His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
 275 280 285
 Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
 290 295 300
 Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
 305 310 315 320
 Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
 325 330 335
 His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
 340 345 350
 Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
 355 360 365
 Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
 370 375 380
 Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Ser Leu Trp
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGATGCC	180
TACCAACCACC	TGGATTCCCTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGCCCAT	GAAGAACCG	GTTGCTGTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCC	GCAGCCTTGG	TAACTATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAAGCAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCCTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCT	CAGGCAGCTG	600
CTCACTTCT	TCGAGAACGG	CGCCGAGCCC	CACGCCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCCAAACG	ACCGGGGCTG	CGGGGAGCCG	CGGCCAACA	CCATGCC	CAACTGCCG	720
CTGCCGCCCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCCTGG	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGG	TTTCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAAC	840
TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCAAAC	TTGTCAGCAA	TGTCAACACC	AGTGTGCT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCAAGC	TAAGATGCGT	TTTCACAGCC	AACTCTTCTC	CCAGGACTGG	1080
CCACACCCCTA	CCTTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCTGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
1 5 10 15
Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
20 25 30
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
35 40 45
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Asp Ala Tyr His His Leu
50 55 60
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
65 70 75 80
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
85 90 95
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
100 105 110
Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
115 120 125
Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
130 135 140
Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
145 150 155 160
Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
165 170 175
Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
180 185 190
Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
195 200 205
Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
210 215 220
Arg Gly Cys Gly Glu Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
225 230 235 240
Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
245 250 255
Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
260 265 270
His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
275 280 285
Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
290 295 300
Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
305 310 315 320
Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
325 330 335
His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
340 345 350
Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
355 360 365
Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
370 375 380
Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Ser Leu Trp

385

390

395

400

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGCGCCGGC	GCAACACCAT	CGCCCCAAC	TGCGCGCTGC	CGCCTGTGGC	CCCCAACTGC	60
CTGGAGCTGC	GGCGCCTCTG	CTTCTCCGAC	CCGCTTGCA	GATCACGCC	GGTGGATTC	120
CAGACCCACT	GCCATCCCAT	GGACATCCTA	GGAACTTGTG	CAACAGAGCA	GTCAGATGT	180
CTACGAGCAT	ACCTGGGGCT	GATTGGGACT	GCCATGACCC	CCAACTTGT	CAGCAATGTC	240
AACACCAGTG	TTGCCTTAAG	CTGCACCTGC	CGAGGCAGTG	GCAACCTGCA	GGAGGGAGTGT	300
GAAATGCTGG	AAGGGTTCTT	CTCCCACAAAC	CCCTGCCCTCA	CGGAGGCCAT	TGCAGCTAAG	360
ATGCGTTTC	ACAGCCAAC	CTTCTCCCAG	GACTGGCCAC	ACCCTACCTT	TGCTGTGATG	420
GCACACCAGA	ATGAAAACCC	TGCTGTGAGG	CCACAGCCCT	GGGTGCCCTC	TCTTTCTCC	480
TGCACGCTTC	CCTTGATTCT	GCTCCTGAGC	CTATGGTAG			519

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val
1				5				10				15			
Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu
				20				25				30			
Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp
				35				40			45				
Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr
				50				55			60				
Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Val	Ser	Asn	Val
				65				70			75			80	
Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu
					85				90			95			
Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys
				100				105			110				
Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe
				115				120			125				
Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met	Ala	His	Gln	Asn
				130				135			140				
Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro	Ser	Leu	Phe	Ser
				145				150			155			160	
Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp				
				165				170							

Figure 1 - SEQ ID NO:1

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1  ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT
51  GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC
101 TTCCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG
151 TGCCAGGCTG ATCCCACCTG CAGTGCTGCC TACCAACCAC TGGATTCCCTG
201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG
251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC
301 TGCATGTGCC ACCGGCGCAT GAAGAACAG GTTGCCTGCT TGGACATCTA
351 TTGGACCGTT CACCGTGCCTC GCAGCCTTGG TAACTATGAG CTGGATGTCT
401 CCCCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC
451 AAACTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCCTA AGTTTGCCAT
501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG
551 AGGCGTGCTC CGGGCCCCAC TGCCAGGCC ACGTCTGCCT CAGGCAGCTG
601 CTCACCTTCT TCGAGAAGGC CGCCGAGCCC CACCGCAGG GCCTGCTACT
651 GTGCCCATGT GCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA
701 CCATCGCCCC CAACTGCGCG CTGCCGCCCTG TGGCCCCCAA CTGCCCTGGAG
751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAAGATCAC GCCTGGTGG
801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC TGTGCAACAG
851 AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG
901 ACCCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTGCTT TAAGCTGCAC
951 CTGCCGAGGC AGTGGCAACC TGCAAGGAGGA GTGTGAAATG CTGGAAGGGT
1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT
1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCCTA CCTTTGCTGT
1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC
1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

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Figure 2 - SEQ ID NO:2

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1  MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK
51  CQADPTCSAA YHHLDSCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG
101 CMCHRRMKNQ VACLDIYWTV HRARSLGNYE LDVSPYEDTV TSKPWKMNL
151 KLNMLKPDSD LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL
201 LTFFEKAEP HAQGLLLCPC APNDRGCCER RRNTIAPNCA LPPVAPNCLE
251 LRRLCFSDPL CRSRLVDFQT HCHPMDILGT CATEQSRLCLR AYLGLIGTAM
301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR
351 FHSQQLFSQDW PHPTFAVMAH QNENPAVRPQ PWVPSLFSCT LPLILLLSLW

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Figure 3 - SEQ ID NO:3

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1  ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT
51  GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC
101 TTCCCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG
151 TGCCAGGCTG ATCCCACCTG CAGTGATGCC TACCACCACC TGGATTCCCTG
201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG
251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC
301 TGCATGTGCC ACCGGCGCAT GAAGAACCAAG GTTGCCTGCT TGGAcATCTA
351 TTGGACCGTT CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT
401 CCCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC
451 AAACTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT
501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG
551 AGGCGTGCTC CGGGCCCCAC TGCCAGGCC ACGTCTGCCT CAGGCAGCTG
601 CTCACTTCTC TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT
651 GTGCCCATGT GCCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA
701 CCATCGCCCC CAACTGCGCG CTGCCGCCCTG TGGCCCCCAA CTGCCTGGAG
751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAGATCAC GCCTGGTGGA
801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC TGTGCAACAG
851 AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG
901 ACCCCCCAACT TTGTCAAGCAA TGTCAACACC AGTGTGCTT TAAGCTGCAC
951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT
1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCCT
1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCCTA CCTTGCTGT
1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC
1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

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Figure 4 - SEQ ID NO:4

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1  MVRPLNPRPL PPVVLMLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK
51  CQADPTCSDA YHILDSCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG
101 CMCHRRMKNQ VACLDIYWTW HRARSLGNYE LDVSPYEDTV TSKPWKMNL
151 KLNMLKPDSD LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL
201 LTFFEKAAEP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCLE
251 LRRLCFSDP CRSRLVDFQT HCHPMDILGT CATEQSRLR AYLGLIGTAM
301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR
351 FHSQQLFSQDW PHPTFAVMAH QNENPAVRPQ PWVPSLFSCT LPLILLSLW

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Figure 5 - SEQ ID NO:5 (Partial coding cDNA sequence for human GDNF $\alpha 3$ receptor)

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1      GAGCGCCGGC GCAACACCAT CGCCCCAAC TGCGCGCTGC CGCCTGTGGC
5
51     CCCCAACTGC CTGGAGCTGC GGCGCCTCTG CTTCTCCGAC CCGCTTGCA
101    GATCACGCCT GGTGGATTTC CAGACCCACT GCCATCCCAT GGACATCCTA
10      151    GGAACTTGTG CAACAGAGCA GTCCAGATGT CTACGAGCAT ACCTGGGGCT
201    GATTGGGACT GCCATGACCC CCAACTTTGT CAGCAATGTC AACACCAGTG
251    TTGCCTTAAG CTGCACCTGC CGAGGCAGTG GCAACCTGCA GGAGGAGTGT
15      301    GAAATGCTGG AAGGGTTCTT CTCCCACAAC CCCTGCCTCA CGGAGGCCAT
351    TGCAGCTAAG ATGCGTTTC ACAGCCAAC TTTCTCCAG GACTGGCCAC
20      401    ACCCTACCTT TGCTGTGATG GCACACCAGA ATGAAAACCC TGCTGTGAGG
451    CCACAGCCCT GGGTGCCCTC TCTTTCTCC TGCACGCTTC CCTTGATTCT
501    GCTCCTGAGC CTATGGTAG
25

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Figure 6 - SEQ ID NO:6 (amino acid sequence for the partial GDNF $\alpha 3$ receptor sequence)

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1      ERRRNTIAPN CALPPVAPNC LELRRLCFSD PLCRSRLVDF QTHCHPMIDIL
30
30      51     GTCATEQSRC LRAYLGLIGT AMTPNFVSNV NTSVALSCTC RGSGNLQEEC
101    EMLEGFFSHN PCLTEAIAAK MRFHSQLFSQ DWPHPTFAVM AHQNENPAVR
35      151    PQPWVPSLFS CTLPLILLLS LW

```

The sequence underlined corresponds to the predicted hydrophobic C-terminus characteristic of GPI anchored cell-surface receptors

Figure 1 - SEQ ID NO:1

1 ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC
 101 TTCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG
 151 TGCCAGGCTG ATCCCACCTG CAGTGCTGCC TACCACCACC TGGATTCTG
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGGAGCCT TCGGTCCCTG
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC
 301 TGCATGTGCC ACCGGCGCAT GAAGAACCCAG GTTGCTGCT TGGAcATCTA
 351 TTGGACCGTT CACCGTGCC GCAGCCTTGG TAACTATGAG CTGGATGTCT
 401 CCCCCATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC
 451 AAACTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT
 501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG
 551 AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG
 601 CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT
 651 GTGCCCATGT GCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA
 701 CCATCGCCCC CAACTGCGCG CTGCCGCTG TGGCCCCAA CTGCCTGGAG
 751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAAGATCAC GCCTGGTGA
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC TGTGCAACAG
 851 AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG
 901 ACCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTGCT TAAGCTGCAC
 951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT
 1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT
 1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCTA CCTTGCTGT
 1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC
 1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

Figure 2 - SEQ ID NO:2

1 MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK
 51 CQADPTCSAA YHHLDSCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG
 101 CMCHRRMKNQ VACLDIYWTW HRARSLGNYE LDVSPYEDTV TSKPWKMNL
 151 KLNMLKPDSD LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL
 201 LTFFEKAAEP HAQGLLLCPC APNDRGCCER RRNTIAPNCA LPPVAPNCL
 251 LRLLCFSDPL CRSRLVDFQT HCHPMIDILGT CATEQSRLCLR AYLGLIGTAM
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR
 351 FHSQQLFSQDW PHPTFAVMAH QNENPAVRPQ PWVPSLFSCT LPLILLLSW

Figure 3 - SEQ ID NO:3

1 ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC
 101 TTCCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG
 151 TGCCAGGCTG ATCCCACCTG CAGTGATGCC TACCACCACC TGGATTCCCTG
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC
 301 TGCATGTGCC ACCGGCGCAT GAAGAACCAAG GTTGCCTGCT TGGAcATCTA
 351 TTGGACCGTT CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT
 401 CCCCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC
 451 AAACTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT
 501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG
 551 AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG
 601 CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT
 651 GTGCCCATGT GCCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA
 701 CCATCGCCCC CAACTGCGCG CTGCCGCCTG TGGCCCCAA CTGCCTGGAG
 751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAGATCAC GCCTGGTGGA
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC TGTGCAACAG
 851 AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG
 901 ACCCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTGCT TAAGCTGCAC
 951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT
 1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT
 1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCCTA CCTTGCTGT
 1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC
 1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

Figure 4 - SEQ ID NO:4

1 MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK
 51 CQADPTCSDA YHLDSCCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG
 101 CMCHRRMKNQ VACLDIYWTW HRARSLGNYE LDVSPYEDTV TSKPWKMNL
 151 KLNMLKPDSD LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL
 201 LTFFEKAEEP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCL
 251 LRRLCFSDPL CRSRLVDFQT HCHPMDILGT CATEQSRLCLR AYLGLIGTAM
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR
 351 FHSQQLFSQDW PHPTFAVMAH QNENPAVRPQ PWVPSLFSCT LPLILLSLW .

Figure 5 - SEQ ID NO:5 (Partial coding cDNA sequence for human GDNF $\alpha 3$ receptor)

1 GAGCGCCGGC GCAACACCAT CGCCCCAAC TGCGCGCTGC CGCCTGTGGC
5
51 CCCCAACTGC CTGGAGCTGC GGCGCCTCTG CTTCTCCGAC CCGCTTGCA
101 GATCACGCCT GGTGGATTTC CAGACCCACT GCCATCCCAT GGACATCCTA
10 151 GGAACTTGTG CAACAGAGCA GTCCAGATGT CTACGAGCAT ACCTGGGCT
201 GATTGGGACT GCCATGACCC CCAACTTGT CAGCAATGTC AACACCAGTG
251 TTGCCTTAAG CTGCACCTGC CGAGGCAGTG GCAACCTGCA GGAGGAGTGT
15
301 GAAATGCTGG AAGGGTTCTT CTCCCACAAC CCCTGCCTCA CGGAGGCCAT
351 TGCAGCTAAG ATGCGTTTC ACAGCCAAC TTTCTCCAG GACTGGCCAC
20 401 ACCCTACCTT TGCTGTGATG GCACACCAGA ATGAAAACCC TGCTGTGAGG
451 CCACAGCCCT GGGTGCCCTC TCTTTCTCC TGCACGCTTC CCTTGATTCT
501 GCTCCTGAGC CTATGGTAG
25

Figure 6 - SEQ ID NO:6 (amino acid sequence for the partial GDNF $\alpha 3$ receptor sequence)

1 ERRRNTIAPN CALPPVAPNC LELRRLCFSD PLCRSRLVDF QTHCHPMIDIL
30
51 GTCATEQSRC LRAYLGLIGT AMTPNFVSNV NTSVALSCTC RGSGNLQEEC
101 EMLEGFFSHN PCLTEAIAAK MRFHSQLFSQ DWPHPTFAVM AHQNENPAVR
35 151 PQPWVPSLFS CTLPLILLLS LW

The sequence underlined corresponds to the predicted hydrophobic C-terminus characteristic of GPI anchored cell-surface receptors